

SEQUENCE LISTING

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Jing, Shuqian

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<151> 2001-06-21

<150> 09/810,384
<151> 2001-03-16

<150> 60/266,159
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Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser
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Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp
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Ser Thr Val Pro Val Pro Leu Glu Pro Ala Arg Pro Asn Arg His
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Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala
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Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro
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Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu
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His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly
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Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu
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Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly
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Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg
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Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys
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Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly
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Val Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys
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Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser
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Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu
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Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp
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Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
115 120 125

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Val Cys Val Arg Pro Arg Val Met Ala
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Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser
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Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
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Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
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Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
50 55 60

Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
65 70 75 80

Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg
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<213> Homo sapiens

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Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg
35 40 45

Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
50 55 60

Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
65 70 75 80

Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg
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Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly Gln Ala Pro
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Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln Ala Leu Pro Val
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Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His Arg Gly Arg His Glu
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Arg Pro Ser Ala Thr Thr Gln Cys Pro Val Leu Arg Pro Glu Glu Val
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Leu Glu Ala Asp Thr His Gln Arg Ser Ile Ser Pro Trp Arg Tyr Arg
100 105 110

Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe Ala Glu
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Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala
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tct gtg tcc ccc cca gag cct ctg agc cac acc cac gca gaa tcc 678
Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu Ser
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tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct cct 726
Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser Pro
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Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr Gly
90 95 100

tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac cag 870
Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn Gln
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Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Gly Thr His Arg
125 130 135

cgc tac tgc ttg gag cgc agg ctc tac cga gtc tcc ttg gct tgt gtg 966
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Cys Val Arg Pro Arg Val Met
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35 40 45

Ser His Thr His His Ala Glu Ser Cys Arg Ala Ser Lys Asp Gly Pro
50 55 60

Leu Asn Ser Arg Ala Ile Ser Pro Trp Ser Tyr Glu Leu Asp Arg Asp
65 70 75 80

Leu Asn Arg Val Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro
85 90 95

His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Leu Gly Asn
100 105 110

Ser Val Pro Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys
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Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
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<210> 11

<211> 27

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Epoegen signal peptide

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<211> 233

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: peptide of Fc fragment

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20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Peptide of HIV
TAT protein

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Peptide of HIV
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
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Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
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Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
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Pro Val Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
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gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346
Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys
85 90 95

gtg agg tgc aat tac aca gag gcc ttc cag act cag acc aga ccc tct 394
Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser
100 105 110 115

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Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
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Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn
135 140 145

gaa gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta 538
Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu
150 155 160

gac cac ata atg aaa tat aaa aag tgt gtc aag gcc gga agc ctg 586
Asp His Ile Met Lys Tyr Lys Lys Cys Val Lys Ala Gly Ser Leu
165 170 175

tgg gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa 634
Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu
180 185 190 195

gtg aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc 682
Val Asn Phe Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile
200 205 210

caa cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag 730
Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln
215 220 225

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Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser
230 235 240

gaa ggt gct acg gtg cag ctg act cca tat ttt cct act tgt ggc agc 826
Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser
245 250 255

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Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly
260 265 270 275

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Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu
280 285 290

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295 300 305

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Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe
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Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro
325 330 335

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Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu
340 345 350 355

caa aac cat tgc aga agt gag gtc atc ctc gaa aag tgg cag aaa aag 1162
Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys
360 365 370

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375 380 385

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390 395 400

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Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser
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Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp. Leu Arg
420 425 430 435

agc cag att cat ctg cac aaa tac gtg gtg gtc tac ttt aga gag att 1402
Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile
440 445 450

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Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His
455 460 465

ctc atg aag gat gcc act gct ttc tgt gca gaa ctt ctc cat gtc aag 1498
Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys
470 475 480

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485 490 495

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Cys Ser Leu
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<213> Homo sapiens

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35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
195 200 205

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
245 250 255

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
260 265 270

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
275 280 285

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
290 295 300

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
305 310 315 320

Thr Ser Phe Ser Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
325 330 335

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
340 345 350

Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
355 360 365

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
370 375 380

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
385 390 395 400

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
405 410 415

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
420 425 430

Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
435 440 445

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
450 455 460

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
465 470 475 480

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
485 490 495

Asp Gly Cys Cys Ser Leu
500

<210> 19

<211> 2015

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50) .. (1729)

<400> 19

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Met Ser Leu
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gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
55 60 65

gta agc tgg gta ctc cgg qca gat gcc agc atc cgc ttg ttg aag gcc 298
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346

Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys
85 90 95

gtg agg ctg gag tgc agt ggt ggc atc atg gct cgc tgc gac ctc aat 394
Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys Asp Leu Asn
100 105 110 115

ctt ctg ggc tca agc gat cgt tct gct tca gcc tcc cga gcg gct ggg 442
Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg Ala Ala Gly
120 125 130

act gca ggc gtg ggc cac cag acc tgg cta att ttt gta gtt ttt gta 490
Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val Val Phe Val
135 140 145

gag ggg ggt ttc acc gtc ttg ctg gtc ttg aat tcc agt gct cag gcg 538
Glu Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser Ala Gln Ala
150 155 160

atc tgc ctg cct cgg ctt ccc aaa gtc ctg gga tta cag tgg aca ttt 586
Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln Trp Thr Phe
165 170 175

tcc tac atc ggc ttc cct gta gag ctg aac aca gtc tat ttc att ggg 634
Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly
180 185 190 195

gcc cat aat att cct aat gca aat atg aat gaa gat ggc cct tcc atg 682
Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met
200 205 210

tct gtg aat ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat 730
Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr
215 220 225

aaa aaa aag tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act 778
Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr
230 235 240

gct tgt aag aag aat gag gag aca gta gaa gtg aac ttc aca acc act 826
Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr
245 250 255

ccc ctg gga aac aga tac atg gct ctt atc cta cac agc act atc atc 874
Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile
260 265 270 275

ggg ttt tct cag gtg ttt gag cca cac cag aag aaa caa acg cga gct 922
Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala
280 285 290

tca gtg gtg att cca gtg act ggg gat agt gaa ggt gct acg gtg cag 970
Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln
295 300 305

ctg act cca tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa 1018
Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys
310 315 320

gga aca gtt gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat 1066
Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp
325 330 335

aac aac aaa agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct 1114
Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Ser
340 345 350 355

ctg ctg gtg gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg 1162
Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp
360 365 370

agg cac gaa agg atc aag aag act tcc ttt tct acc acc aca cta ctg 1210
Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu
375 380 385

ccc ccc att aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat 1258
Pro Pro Ile Lys Val Leu Val Tyr Pro Ser Glu Ile Cys Phe His
390 395 400

cac aca att tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt 1306
His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser
405 410 415

gag gtc atc ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt 1354
Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Ile Ala Glu Met Gly
420 425 430 435

cca gtg cag tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc 1402
Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val
440 445 450

tcc ctt ctt tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc 1450
Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly
455 460 465

aag agc gag ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt 1498
Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu
470 475 480

gcc ttt aac ctt ttc tgc agt gat cta aga agc cag att cat ctg cac 1546
Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His
485 490 495

aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac 1594
Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr
500 505 510 515

aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act 1642
Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr
520 525 530

gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga 1690
Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly
535 540 545

aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccccaccc 1739
Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
550 555 560

atgagaagca agagaccta aaggcttctt atcccaccaa ttacaggaa aaaaacgtgtg 1799

atgatcctga agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac 1859

caataaaaatt ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaaactacat 1919

ttacaacttc aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta 1979
accatttga taatgcaaca ataaaggcatc ttccagc 2015

<210> 20
<211> 560
<212> PRT
<213> Homo sapiens

<400> 20
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
100 105 110

Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
115 120 125

Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
130 135 140

Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
145 150 155 160

Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175

Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190

Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205

Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220

Met Lys Tyr Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240

Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255

Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
260 265 270

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
290 295 300

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
305 310 315 320

Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
325 330 335

Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu
340 345 350

Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr
355 360 365

Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr
370 375 380

Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile
385 390 395 400

Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His
405 410 415

Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala
420 425 430

Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp
435 440 445

Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly
450 455 460

Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu
465 470 475 480

Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile
485 490 495

His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys
500 505 510

Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys
515 520 525

Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val
530 535 540

Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
545 550 555 560

<210> 21
<211> 521
<212> PRT
<213> Homo sapiens

<400> 21
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Ser
100 105 110

Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
115 120 125

Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn
130 135 140

Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu
145 150 155 160

Asp His Ile Met Lys Tyr Lys Lys Cys Val Lys Ala Gly Ser Leu
165 170 175

Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu
180 185 190

Val Asn Phe Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile
195 200 205

Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln
210 215 220

Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser
225 230 235 240

Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser
245 250 255

Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly
260 265 270

Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu
275 280 285

Pro Ala Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
290 295 300

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
305 310 315 320

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
325 330 335

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
340 345 350

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
355 360 365

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
370 375 380

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
385 390 395 400

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
405 410 415

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
420 425 430

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
435 440 445

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
450 455 460

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
465 470 475 480

Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
485 490 495

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
500 505 510

Lys Ser Leu Ser Leu Ser Pro Gly Lys
515 520

DNA
<210> 22

<211> 585

<212> PRT

<213> Homo sapiens

<400> 22

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
100 105 110

Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
115 120 125

Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
130 135 140

Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
145 150 155 160

Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175

Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190

Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205

Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220

Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240

Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255

Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
260 265 270

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
290 295 300

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
305 310 315 320

Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
325 330 335

Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala
340 345 350

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
355 360 365

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
370 375 380

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
385 390 395 400

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
405 410 415

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
420 425 430

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
435 440 445

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
450 455 460

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys
580 585

<210> 23

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

gtacagtggc tgaccactca gaag

24

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24

ggtggactac aagggtgaac agc

23